Deciphering the genomic diversity of Bombyx mori nucleopolyhedrovirus isolates from Southeast Asia

Sergei Senger
Julius Kühn Institute, Institute for Biological Control, Darmstadt
E-mail of corresponding author: sergei.senger@web.de

The main source of silk in the wolrd stems from the larvae of *Bombyx mori*, the domestic silkworm. In this report ten isolates of the Bombyx mori nucleopolyhedrovirus (BmNPV) of the family Baculoviridae, genus Alphabaculovirus, from different geographic areas of India and Thailand were deciphered for their genetic composition by analyzing specific single nucleotide polymorphisms (SNPs). An alignment free method was used, where the generation of consensus sequences from the sequencing data was avoided to the greatest possible extent. The quantification of mixtures was done by a so-called quantitative SNP analysis where isolate specific variant positions were used. This method had been successfully applied on isolates of the Cydia pomonella granulovirus, genus Betabaculovirus, and was tested, for the first time, on a member of the genus Alphabaculovirus, namely BmNPV. Based on quantitative SNP analysis of the Indian isolates, a homogenous isolate (BmNPV-My) and two mixed isolates (BmNPV-De and BmNPV-Ja) were identified. The mixtures were about equal parts of BmNPV-My and BmNPV-De/Ja, with the latter two appearing to be highly similar. Thai isolates also included mixtures and pure genotypes, but were harder to decipher. Phylogenetic studies also showed a strong correlation between the distance of BmNPVs and their genetic similarities.